



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(54) Title: <b>NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI AND VACCINE COMPOSITIONS THEREOF</b>			
(57) Abstract			
Recombinant or substantially pure preparations of <i>H. pylori</i> polypeptides are described. The nucleic acids encoding the polypeptides also are described. The <i>H. pylori</i> polypeptides are useful in diagnostic and vaccine compositions.			

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**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
HELICOBACTER PYLORI AND VACCINE COMPOSITIONS THEREOF**

Background of the Invention

5           *Helicobacter pylori* is a gram-negative, S-shaped, microaerophilic bacterium that was discovered and cultured from a human gastric biopsy specimen. (Warren, J.R. and B. Marshall, (1983) *Lancet* 1: 1273-1275; and Marshall et al., (1984) *Microbios Lett.* 25: 83-88). *H. pylori* has been strongly linked to chronic gastritis and duodenal ulcer disease. (Rathbone et. al., (1986) *Gut* 27: 635-641). Moreover, evidence is  
10 accumulating for an etiologic role of *H. pylori* in nonulcer dyspepsia, gastric ulcer disease, and gastric adenocarcinoma. (Blaser M. J., (1993) *Trends Microbiol.* 1: 255-260). Transmission of the bacteria occurs via the oral route, and the risk of infection increases with age. (Taylor, D.N. and M. J. Blaser, (1991) *Epidemiol. Rev* 13: 42-50). *H. pylori* colonizes the human gastric mucosa, establishing an infection that usually  
15 persists for decades. Infection by *H. pylori* is prevalent worldwide. Developed countries have infection rates over 50% of the adult population, while developing countries have infection rates reaching 90% of the adults over the age of 20. (Hopkins R. J. and J. G. Morris (1994) *Am. J. Med.* 97: 265-277).

          The bacterial factors necessary for colonization of the gastric environment, and  
20 for virulence of this pathogen, are poorly understood. Examples of the putative virulence factors include the following: urease, an enzyme that may play a role in neutralizing gastric acid pH (Eaton et al., (1991) *Infect. Immunol.* 59: 2470-2475; Ferrero, R.L. and A. Lee (1991) *Microb. Ecol. Hlth. Dis.* 4: 121-134; Labigne et al., (1991) *J. Bacteriol.* 173: 1920-1931); the bacterial flagellar proteins responsible for  
25 motility across the mucous layer. (Hazell et al., (1986) *J. Inf. Dis.* 153: 658-663; Leying et al., (1992) *Mol. Microbiol.* 6: 2863-2874; and Haas et al., (1993) *Mol. Microbiol.* 8: 753-760); Vac A, a bacterial toxin that induces the formation of intracellular vacuoles in epithelial cells (Schmitt, W. and R. Haas, (1994) *Molecular Microbiol.* 12(2): 307-319); and several gastric tissue-specific adhesins. (Boren et al., (1993) *Science* 262: 1892-  
30 1895; Evans et al., (1993) *J. Bacteriol.* 175: 674-683; and Falk et al., (1993) *Proc. Natl. Acad. Sci. USA* 90: 2035-2033).

          Numerous therapeutic agents are currently available that eradicate *H. pylori* infections *in vitro*. (Huesca et. al., (1993) *Zbl. Bakt.* 280: 244-252; Hopkins, R. J. and J. G. Morris, supra). However, many of these treatments are suboptimally effective *in vivo*  
35 because of bacterial resistance, altered drug distribution, patient non-compliance or poor drug availability. (Hopkins, R. J. and J. G. Morris, supra). Treatment with antibiotics combined with bismuth are part of the standard regime used to treat *H. pylori* infection.

(Malfertheiner, P. and J. E. Dominguez-Munoz (1993) *Clinical Therapeutics* 15 Supp. B: 37-48). Recently, combinations of a proton pump inhibitors and a single antibiotic have been shown to ameliorate duodenal ulcer disease. (Malfertheiner, P. and J. E. Dominguez-Munoz supra). However, methods employing antibiotic agents can have the  
5 problem of the emergence of bacterial strains which are resistant to these agents. (Hopkins, R. J. and J. G. Morris, supra). These limitations demonstrate that new more effective methods are needed to combat *H. pylori* infections *in vivo*. In particular, the design of new vaccines that may prevent infection by this bacterium is highly desirable.

#### 10 Summary of the Invention

This invention relates to novel genes, e.g., genes encoding polypeptides such as bacterial surface proteins, from the organism *Helicobacter pylori* (*H. pylori*), and other related genes, their products, and uses thereof. The nucleic acids and peptides of the present invention have utility for diagnostic and therapeutics for *H. pylori* and other  
15 *Helicobacter* species. They can also be used to detect the presence of *H. pylori* and other *Helicobacter* species in a sample; and for use in screening compounds for the ability to interfere with the *H. pylori* life cycle or to inhibit *H. pylori* infection. More specifically, this invention features compositions of nucleic acids corresponding to entire coding sequences of *H. pylori* proteins, including surface or secreted proteins or  
20 parts thereof, nucleic acids capable of binding mRNA from *H. pylori* proteins to block protein translation, and methods for producing *H. pylori* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to detect *H. pylori* infection. In addition, vaccine compositions and methods for the protection against infection by *H. pylori* are  
25 within the scope of this invention.

#### Detailed Description of the Drawings

Figure 1 is a bar graph that depicts the antibody titer in serum of mice following immunization with specific *H. pylori* antigens.

30 Figure 2 is a bar graph that depicts the antibody titer in mucous of mice following immunization with specific *H. pylori* antigens.

Figure 3 is a bar graph that depicts therapeutic immunization of *H. pylori* infected mice with specific antigens dissolved in HEPES buffer.

Figure 4 is a bar graph that depicts therapeutic immunization of *H. pylori*  
35 infected mice with specific antigens dissolved in buffer containing DOC.

Figure 5 is a graph depicting the activity of recombinant PPIase.

Figure 6 is a graph depicting PPIase activity in an *H. pylori* extract.

Figure 7 is a graph depicting a decrease of glutamate racemase activity with L-Serine-O-Sulfate.

Figure 8 depicts the amino acid sequence alignment in a portion of the sequence of 12 *H. pylori* proteins (depicted in the single letter amino acid code and designated by their amino acid Sequence ID Numbers; shown N-terminal to C-terminal, left to right).

Figure 9 depicts the N-terminal portion of nine *H. pylori* proteins (depicted in the single letter amino acid code and designated by their amino acid Sequence ID Numbers; shown N-terminal to C-terminal, left to right).

#### Detailed Description of the Invention

In one aspect, the invention features a recombinant or substantially pure preparation of *H. pylori* polypeptide of SEQ ID NO: 492. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide of SEQ ID NO: 492, such nucleic acid is contained in SEQ ID NO: 1. The *H. pylori* polypeptide sequences described herein are contained in the Sequence Listing, and the nucleic acids encoding *H. pylori* polypeptides are contained in the Sequence Listing.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 492 through SEQ ID NO: 541. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 492 through SEQ ID NO: 541, such nucleic acids are contained in SEQ ID NO: 1 through SEQ ID NO: 50.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 542 through SEQ ID NO: 591. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 542 through SEQ ID NO: 591, such nucleic acids are contained in SEQ ID NO: 51 through SEQ ID NO: 100.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 592 through SEQ ID NO: 641. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 592 through SEQ ID NO: 641, such nucleic acids are contained in SEQ ID NO: 101 through SEQ ID NO: 150.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 642 through SEQ ID NO: 691. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 642 through SEQ ID NO: 691, such nucleic acids are contained in SEQ ID NO: 151 through SEQ ID NO: 200.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 692 through SEQ ID NO: 741. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 692 through SEQ ID NO: 741, such nucleic acids are contained in SEQ ID NO: 201 through SEQ ID NO: 250.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 742 through SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765 through SEQ ID NO: 791. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 742 through SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765 through SEQ ID NO: 791, such nucleic acids are contained in SEQ ID NO: 251 through SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, and SEQ ID NO: 274 through SEQ ID NO: 300.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 792 through SEQ ID NO: 818 and SEQ ID NO: 820 through SEQ ID NO: 841. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 792 through SEQ ID NO: 818 and SEQ ID NO: 820 through SEQ ID NO: 841, such nucleic acids are contained in SEQ ID NO: 301 through SEQ ID NO: 327 and SEQ ID NO: 329 through SEQ ID NO: 350.

In another aspect, the invention features a recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides of SEQ ID NO: 842 through SEQ ID NO: 846 and SEQ ID NO: 848 through SEQ ID NO: 891. The invention also includes substantially pure nucleic acid encoding an *H. pylori* polypeptide selected from the group consisting of *H. pylori* polypeptides SEQ ID NO: 842 through SEQ ID NO: 846 and SEQ ID NO: 848 through

991

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Arg Ile Gln Arg Phe Leu Ser Arg Lys Met Ala Gln Lys Lys Gly Glu
   35           40           45
Lys Leu Lys Leu Ala Pro Tyr Glu Cys Gly Pro Val Ala Leu Lys Gln
   50           55           60
Pro Asn Arg Val Ser His His Phe Tyr Ile Met Ala Met Leu Phe Ile
  65           70           75           80
Leu Phe Asp Val Glu Ile Val Phe Met Phe Pro Trp Ala Ile Asp Phe
           85           90           95
Lys Lys Leu Gly Leu Phe Gly Leu Val Glu Met Leu Gly Phe Val Phe
          100          105          110
Phe Leu Ala Ile Gly Phe Ile Tyr Ala Leu Lys Arg Asn Ala Leu Ser
          115          120          125
Trp Gln Lys Leu Glu Val Lys
          130          135

```

## (2) INFORMATION FOR SEQ ID NO:1077:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...635

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

```

Leu Ser Ser Asp Pro Ser Ala Val Asn Asp Ala Arg Asp Asn Leu Gly
1           5           10           15
Ser Ser Thr Arg Asn Leu Leu Asp Val Lys Ala Asn Ser Pro Ala Tyr
          20          25          30
Gln Ala Val Leu Leu Ala Leu Asn Ala Ala Val Gly Leu Trp Gln Val
          35          40          45
Thr Ser Tyr Ala Phe Thr Ala Cys Gly Pro Gly Ser Asn Glu Asn Ala
          50          55          60
Asn Gly Gly Ile Gln Thr Phe Asn Asn Val Pro Gly Gln Asn Thr Thr
  65           70           75           80
Thr Ile Thr Cys Asn Ser Tyr Tyr Glu Pro Gly His Gly Gly Pro Ile
          85          90          95
Ser Thr Lys Asn Tyr Ala Ile Ile Asn Lys Ala Tyr Gln Ile Ile Gln
          100         105         110
Lys Ala Leu Thr Ala Asn Gly Glu Gly Ile Pro Val Leu Ser Asn Thr
          115         120         125
Thr Thr Lys Leu Asp Phe Thr Ile Asn Gly Asp Lys Arg Thr Gly Gly
          130         135         140
Glu Pro Asn Lys Lys Leu Val Tyr Pro Trp Ser His Gly Lys Ala Ile
 145          150          155          160
Ser Thr Ser Trp Asn Ala Thr Ile Thr Ala Pro Thr Thr Glu Asn Ile
          165          170          175

```

Asn Thr Thr Asn Ser Ala Gln Glu Leu Leu Lys Gln Ala Ser Ile Ile  
 180 185 190  
 Ile Thr Thr Leu Asn Ser Ala Cys Pro Asn Phe Gln Asn Gly Gly Ser  
 195 200 205  
 Gly Tyr Trp Ala Gly Ile Ser Gly Asn Gly Thr Met Cys Gly Met Phe  
 210 215 220  
 Lys Asn Glu Ile Ser Ala Ile Gln Gly Met Ile Ala Asn Ala Gln Glu  
 225 230 235 240  
 Ala Val Ala Gln Ala Lys Ile Val Ser Glu Asn Thr Gln Asn Gln Asn  
 245 250 255  
 Ser Leu Asp Ala Gly Lys Pro Phe Asn Pro Tyr Thr Asp Ala Ser Phe  
 260 265 270  
 Ala Glu Ser Met Leu Lys Asn Ala Gln Ala Gln Ala Glu Ile Leu Asn  
 275 280 285  
 Gln Ala Glu Gln Val Val Lys Asn Phe Glu Lys Ile Pro Thr Ala Phe  
 290 295 300  
 Val Asn Asp Ser Leu Gly Val Cys Tyr Glu Val Gln Gly Gly Glu Arg  
 305 310 315 320  
 Arg Gly Thr Asn Pro Gly Gln Thr Thr Ser Asn Thr Trp Gly Ala Gly  
 325 330 335  
 Cys Ala Tyr Val Gly Gln Thr Ile Thr Asn Leu Lys Asn Ser Ile Ala  
 340 345 350  
 His Phe Gly Thr Gln Glu Gln Gln Ile Gln Gln Ala Glu Asn Ile Ala  
 355 360 365  
 Asp Thr Leu Val Asn Phe Lys Ser Arg Tyr Ser Glu Leu Gly Asn Thr  
 370 375 380  
 Tyr Asn Ser Ile Thr Thr Ala Leu Ser Asn Ile Pro Asn Ala Gln Ser  
 385 390 395 400  
 Leu Gln Asn Ala Val Ser Lys Lys Asn Asn Pro Tyr Ser Pro Gln Gly  
 405 410 415  
 Ile Asp Thr Asn Tyr Tyr Leu Asn Gln Asn Ser Tyr Asn Gln Ile Gln  
 420 425 430  
 Thr Ile Asn Gln Glu Leu Gly Arg Asn Pro Phe Arg Lys Val Gly Ile  
 435 440 445  
 Val Ser Ser Gln Thr Asn Asn Gly Ala Met Asn Gly Ile Gly Ile Gln  
 450 455 460  
 Val Gly Tyr Lys Gln Phe Phe Gly Gln Lys Arg Lys Trp Gly Ala Arg  
 465 470 475 480  
 Tyr Tyr Gly Phe Phe Asp Tyr Asn His Ala Phe Ile Lys Ser Ser Phe  
 485 490 495  
 Phe Asn Ser Ala Ser Asp Val Trp Thr Tyr Gly Phe Gly Ala Asp Ala  
 500 505 510  
 Leu Tyr Asn Phe Ile Asn Asp Lys Ala Thr Asn Phe Leu Gly Lys Asn  
 515 520 525  
 Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Ala Leu Ala Gly Thr  
 530 535 540  
 Ser Trp Leu Asn Ser Glu Tyr Val Asn Leu Ala Thr Met Asn Asn Val  
 545 550 555 560  
 Tyr Asn Ala Lys Met Asn Val Ala Asn Phe Gln Phe Leu Phe Asn Met  
 565 570 575  
 Gly Val Arg Met Asn Leu Ala Arg Pro Lys Lys Lys Asp Ser Asp His  
 580 585 590  
 Ala Ala Gln His Gly Ile Glu Leu Gly Leu Lys Ile Pro Thr Ile Asn  
 595 600 605  
 Thr Asn Tyr Tyr Ser Phe Met Gly Ala Glu Leu Lys Tyr Arg Arg Leu  
 610 615 620  
 Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr



625

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## (2) INFORMATION FOR SEQ ID NO:1078:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...174

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

```

Ile Lys Arg Ile Ile Lys Ser Asn Ala Ser Leu Asn Gln Leu Asn Thr
1      5      10      15
Thr Arg Tyr Asn Thr Pro Ser His Leu Phe Phe Lys Lys Gly Val Gly
      20      25      30
Met Ala Thr Ile Gln Pro Phe Asn His Ser Thr Ile Gln Pro Phe Asn
      35      40      45
His Ser Thr Ile Gln Pro Phe Asn His Ser Ile Ile Gln Ser Phe Asn
      50      55      60
His Ser Thr Ile Gln Ala Thr Leu Pro Tyr Phe Tyr Asn Tyr Leu Ser
65      70      75      80
Phe Tyr Lys Asn Leu Phe Lys Asn Pro Leu Phe Phe Ile Ile Pro Pro
      85      90      95
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
      100     105     110
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
      115     120     125
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro
      130     135     140
Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Asn Pro Phe Ile Ser Pro
145     150     155     160
Ser Leu Thr His Ala Thr Thr Phe Ser Asn His Leu Ile Pro
      165     170

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## (2) INFORMATION FOR SEQ ID NO:1079:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```

Met Glu Asp Phe Leu Tyr Asn Thr Leu Tyr Phe Ile Glu Asp Tyr Lys
1      5      10      15
Leu Val Val Ile Phe Ser Phe Ile Gly Leu Ile Ala Leu Phe Phe Leu
20      25      30
Tyr Lys Phe Ile Lys Thr Gln Lys Lys Val Phe Lys Asp Lys Ala Asn
35      40      45
Gln Pro Gln Lys Lys Lys Ser Phe Lys Glu Ile Ile Ile Asp Gly Leu
50      55      60
Lys Glu Arg Val Lys Thr Phe Gly Phe Trp Leu Gln Ala Ile Leu Leu
65      70      75      80
Leu Ser Tyr Ser Phe Ile Thr Ser Gly Leu Phe Phe Leu Ile Leu Leu
85      90      95
Gly Asn Phe Tyr Asp Asp Asn Arg Leu Pro Glu Ser Asp Asp Asp Leu
100     105     110
Phe Asp Ile Trp Val Tyr Ala Ile Gln Asp Phe Pro Ala Tyr Tyr Phe
115     120     125
Lys Ala Leu Thr Phe Ser Ser Leu Lys Ile Tyr Gly Phe Asn Ile Ser
130     135     140
Leu Val Val Tyr Ser Ser Ile Leu Cys Ser Tyr Ile Phe Ile Thr Phe
145     150     155     160
Phe Val Trp Phe Leu Lys Tyr Leu Thr Arg Thr Arg Asp Ile Gly Ala
165     170     175
Asn Lys Lys Val Asp Asp Leu Phe Gly Ser Ala Ser Trp Glu Thr Glu
180     185     190
Glu Lys Met Ile Lys Ala Lys Leu Ile Thr Pro Asn Asn Lys Lys Arg
195     200     205
Ala Phe Asp Lys Arg Glu Val Ile Val Gly Arg Arg Gly Leu Gly Asp
210     215     220
Phe Ile Ala Tyr Ala Gly Gln Ala Phe Ile Gly Leu Ile Ala Pro Thr
225     230     235     240
Arg Ser Gly Lys Gly Val Gly Phe Ile Met Pro Asn Met Ile Asn Tyr
245     250     255
Pro Gln Asn Ile Val Val Phe Asp Pro Lys Ala Asp Thr Met Glu Thr
260     265     270
Cys Gly Lys Ile Arg Glu Lys Arg Phe Asn Gln Lys Val Phe Ile Tyr
275     280     285
Glu Pro Phe Ser Leu Lys Thr His Arg Phe Asn Pro Phe Ala Tyr Val
290     295     300
Asp Phe Gly Asn Asp Val Val Leu Thr Glu Asp Ile Leu Ser Gln Ile
305     310     315     320
Asp Thr Arg Leu Lys Gly His Gly Met Val Ala Ser Gly Gly Asp Phe
325     330     335
Ser Thr Gln Ile Phe Gly Leu Ala Lys Leu Val Phe Pro Glu Arg Pro
340     345     350
Asn Glu Lys Asp Pro Phe Phe Ser Asn Gln Ala Arg Asn Leu Phe Val
355     360     365
Ile Asn Cys Asn Ile Tyr Arg Asp Leu Met Trp Thr Lys Lys Gly Leu
370     375     380
Glu Phe Val Lys Arg Lys Lys Ile Ile Met Pro Glu Thr Pro Thr Met

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ATCTACAACA CCGCGCAAGC TGTATCACT TCAGTATTGG CTTTTTGGAG TCTTTATGCA 360
GGGAACGCTC TCAGTTTTC A TGTGACCGGT TTGAATGATG GATCTAATTC TCCTTTAGGA 420
AGAATCCATA GAGATGGGAA CTGCACAGGA TTACAACAAT GTTTTATGAG CAAAGAAACT 480
TATGATAAAA TGAAGACACT TGCCGAAAAC CTCCAAAAG CTCAAGGCAA TCTCTGTGCC 540
TTATCAGAAT GCTCTAGCAA TCAATCAAAT GGAGGCAAAA CTTCCATGAC TACAGCTCTT 600
CAAACCGCGC AACAGCTCAT GGA CTTAATC GAACAGACCA AGGTTTCTAT GGTGTGGAAA 660
AATATCGTCA TCGCAGGTGT TACAAACAAA CCCAATGGTG CTGGCGCTAT CACATCCACT 720
GGTCATGTAA CCGACTATGC GGTGTTTAA ACATCAAGG CGATGCTACC TATCTTGCAA 780
CAAGCGCTTA CGCTTTCTCA AAGTAACCAC ACCCTATCCA CTCAGTTGCA AGTCGAGCT 840
ATGGGATCTC AAACAAATCG TGAATTCGCT AAAGACATCT ACGCTTTAGC TCAAAACCAA 900
AAGCAAATCC TTTCTAACGC TTCAAGTATC TTCAATCTCT TTAATTCCAT TCCTAAAGAC 960
CAACTTAAGT ATTTGGAGAA CGCTTACTTG AAAGTGCCAC ATTTGGGTAA AACCCTACT 1020
AACCCTTACA GACAGAATGT GAATTTGAAT AAAGAAATTA ATGCGGTTCA AGACAATGTA 1080
GCTAATTATG GTAATCGTTT GGATTCGGCT TTAAGCGTGG CTAAAGATGT TTATAACCTA 1140
AAATCCAATC AAACAGAGAT CGTAACCACT TATAACGATG CTAAGAATTT GAGCGAAGAG 1200
ATTTCTAAAC TTCCCTATAA CCAAGTCAAT GTAACAAACA TCGTTATGTC GCCTAAAGAT 1260
TCTACAGCGG GCCAATACCA AATCAACCCA GAGCAGCAAT CCAATCTTAA CCAAGCTTTA 1320
GCGGCGATGA GCAATAACCC CTTTAAAAAA GTGGGCATGA TCAGCTCTCA AAACAATAAC 1380
GGCGCTTTGA ACGGCTTGG CGTGCAAGTG GGTATAAAC AATTCTTTGG CGAAAGC AAA 1440
AGATGGGGGT TAAGGTATTA TGGTTTCTTT GATTACAACC ACGGCTATAT CAAATCCAGC 1500
TTTTTTAATT CTTCTTCTGA TATATGGACT TATGGCGGTG GGAGCGATT GTTAGTGAAT 1560
TTTATCAACG ATAGCATCAC AAGAAAGAAC AACAAGCTTT CTGTGGGTCT TTTTGGTGGT 1620
ATCCAAC TAG CAGGGACTAC ATGGCTTAAT TCTCAATACA TGAATTTAAC AGCGTTCAAT 1680
AACCCTTACA GCGCGAAAGT CAATGCTTCC AATTTCCAAT TTTTGTTCAA TCTCGGCTTG 1740
AGGACGAATC TCGCTACAGC TAAGAAAAAA GACAGCGAAC GTTCCGCGCA ACATGGCGTT 1800
GAACTGGGCA TTAAATCCC TACCATTAAC ACCAATTATT ATTCTTTTCT AGGCACTAAG 1860
CTAGAATACC GAAGGCTTTA TAGCGTGTAT CTCAATTATG TGTTTGCTTA TTAA 1914

```

## (2) INFORMATION FOR SEQ ID NO:1296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 897 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...897

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

```

Met Glu Gln Pro Val Ile Lys Glu Gly Thr Leu Ala Leu Ile Asp Thr
1           5           10           15
Phe Ala Tyr Leu Phe Arg Ser Tyr Tyr Met Ser Ala Lys Asn Lys Pro
20           25           30
Leu Thr Asn Asp Lys Gly Phe Pro Thr Gly Leu Leu Thr Gly Leu Val
35           40           45
Gly Met Val Lys Lys Phe Tyr Lys Asp Arg Lys Asn Met Pro Phe Ile
50           55           60
Val Phe Ala Leu Glu Ser Gln Thr Lys Thr Lys Arg Ala Glu Lys Leu

```

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65		70		75		80									
Gly	Glu	Tyr	Lys	Gln	Asn	Arg	Lys	Asp	Ala	Pro	Lys	Glu	Met	Leu	Leu
			85					90					95		
Gln	Ile	Pro	Ile	Ala	Leu	Glu	Trp	Leu	Gln	Lys	Met	Gly	Phe	Thr	Cys
		100					105					110			
Val	Glu	Val	Gly	Gly	Phe	Glu	Ala	Asp	Asp	Val	Ile	Ala	Ser	Leu	Ala
		115				120					125				
Thr	Leu	Ser	Pro	Tyr	Lys	Thr	Arg	Ile	Tyr	Ser	Lys	Asp	Lys	Asp	Phe
	130					135					140				
Asn	Gln	Leu	Leu	Ser	Asp	Lys	Ile	Ala	Leu	Phe	Asp	Gly	Lys	Thr	Glu
145				150						155				160	
Phe	Leu	Ala	Lys	Asp	Cys	Val	Glu	Lys	Tyr	Gly	Ile	Leu	Pro	Ser	Gln
			165						170					175	
Phe	Thr	Asp	Tyr	Gln	Gly	Ile	Val	Gly	Asp	Ser	Ser	Asp	Asn	Tyr	Lys
		180						185					190		
Gly	Val	Lys	Gly	Ile	Gly	Ser	Lys	Asn	Ala	Lys	Glu	Leu	Leu	Gln	Arg
	195						200					205			
Leu	Gly	Ser	Leu	Glu	Lys	Ile	Tyr	Glu	Asn	Leu	Asp	Leu	Ala	Lys	Asn
	210					215					220				
Leu	Leu	Ser	Pro	Lys	Met	Tyr	Gln	Ala	Leu	Ile	Gln	Asp	Lys	Gly	Ser
225				230						235				240	
Ala	Phe	Leu	Ser	Lys	Glu	Leu	Ala	Thr	Leu	Glu	Arg	Gly	Cys	Ile	Lys
			245						250					255	
Glu	Phe	Asp	Phe	Leu	Ser	Cys	Ala	Phe	Pro	Ser	Glu	Asn	Pro	Leu	Leu
		260						265					270		
Lys	Ile	Lys	Asp	Glu	Leu	Lys	Glu	Tyr	Gly	Phe	Ile	Ser	Thr	Leu	Arg
	275					280							285		
Asp	Leu	Glu	Asn	Ser	Pro	Phe	Ile	Val	Glu	Asn	Val	Pro	Ile	Leu	Asn
	290					295					300				
Ser	Thr	Pro	Ile	Leu	Asp	Asn	Thr	Pro	Ala	Leu	Asp	Asn	Ala	Pro	Lys
305				310						315				320	
Lys	Ser	Arg	Met	Ile	Val	Leu	Glu	Ser	Ala	Glu	Pro	Leu	Ser	Met	Phe
			325						330					335	
Leu	Glu	Lys	Leu	Glu	Asn	Pro	Asn	Ala	Arg	Val	Phe	Met	Arg	Leu	Val
		340						345					350		
Leu	Asp	Lys	Asp	Lys	Lys	Ile	Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gln	Asp
	355						360					365			
Gln	Gly	Tyr	Phe	Leu	Pro	Leu	Glu	Glu	Ala	Leu	Phe	Ser	Pro	Phe	Ser
	370					375					380				
Leu	Glu	Phe	Leu	Gln	Asn	Ala	Phe	Ser	Gln	Met	Leu	Gln	His	Ala	Cys
385				390						395				400	
Ile	Ile	Gly	His	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Phe	Leu	Lys	Ala	Lys
			405					410						415	
Tyr	Gln	Val	Pro	Leu	Glu	Asn	Ile	Arg	Ile	Gln	Asp	Thr	Gln	Ile	Leu
		420						425					430		
Ala	Phe	Leu	Lys	Asn	Pro	Glu	Lys	Val	Gly	Phe	Asp	Glu	Val	Leu	Lys
	435						440					445			
Glu	Tyr	Leu	Lys	Glu	Asp	Leu	Ile	Pro	His	Glu	Lys	Ile	Lys	Asp	Phe
	450					455					460				
Lys	Thr	Lys	Ser	Lys	Ala	Glu	Lys	Ser	Glu	Leu	Leu	Ser	Met	Glu	Leu
465				470						475				480	
Asn	Ala	Leu	Lys	Arg	Leu	Cys	Glu	Tyr	Phe	Glu	Lys	Gly	Gly	Leu	Glu
			485						490					495	
Glu	Asp	Leu	Leu	Thr	Leu	Ala	Arg	Asp	Ile	Glu	Thr	Pro	Phe	Val	Lys
		500						505					510		
Val	Leu	Met	Gly	Met	Glu	Phe	Gln	Gly	Phe	Lys	Ile	Asp	Ala	Pro	Tyr
		515					520						525		

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Phe Lys Arg Leu Glu Gln Glu Phe Lys Asn Glu Leu Asn Val Leu Glu  
 530 535 540  
 Arg Gln Ile Leu Asp Leu Ile Gly Val Asp Phe Asn Leu Asn Ser Pro  
 545 550 555 560  
 Lys Gln Leu Gly Glu Val Leu Tyr Asp Lys Leu Gly Leu Pro Lys Asn  
 565 570 575  
 Lys Ser His Ser Thr Asp Glu Lys Asn Leu Leu Lys Ile Leu Asp Lys  
 580 585 590  
 His Pro Ser Ile Pro Leu Ile Leu Glu Tyr Arg Glu Leu Asn Lys Leu  
 595 600 605  
 Phe Asn Thr Tyr Thr Thr Pro Leu Leu Arg Leu Lys Asp Lys Asp Asp  
 610 615 620  
 Lys Ile His Thr Thr Phe Ile Gln Thr Gly Thr Ala Thr Gly Arg Leu  
 625 630 635 640  
 Ser Ser His Ser Pro Asn Leu Gln Asn Ile Pro Val Arg Ser Pro Lys  
 645 650 655  
 Gly Leu Leu Ile Arg Lys Gly Phe Ile Ala Ser Ser Lys Glu Tyr Cys  
 660 665 670  
 Leu Leu Gly Val Asp Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His  
 675 680 685  
 Phe Ser Gln Asp Lys Asp Leu Met Glu Ala Phe Leu Lys Gly Arg Asp  
 690 695 700  
 Ile His Leu Glu Thr Ser Lys Ala Leu Phe Gly Glu Asp Leu Ala Lys  
 705 710 715 720  
 Glu Lys Arg Ser Ile Ala Lys Ser Ile Asn Phe Gly Leu Val Tyr Gly  
 725 730 735  
 Met Gly Ser Lys Lys Leu Ser Glu Thr Leu Ser Ile Pro Leu Ser Glu  
 740 745 750  
 Ala Lys Ser Tyr Ile Glu Ala Tyr Phe Lys Arg Phe Pro Ser Ile Lys  
 755 760 765  
 Asp Tyr Leu Asn Gly Met Arg Glu Glu Ile Leu Lys Thr Ser Lys Ala  
 770 775 780  
 Phe Thr Leu Leu Gly Arg Tyr Arg Val Phe Asp Phe Thr Gly Val Asn  
 785 790 795 800  
 Asp Tyr Val Lys Gly Asn Tyr Leu Arg Glu Gly Val Asn Ala Ile Phe  
 805 810 815  
 Gln Gly Ser Ala Ser Asp Leu Leu Lys Leu Gly Met Leu Lys Val Ser  
 820 825 830  
 Glu Arg Phe Lys Asn Asn Pro Ser Val Arg Leu Leu Leu Gln Val His  
 835 840 845  
 Asp Glu Leu Ile Phe Glu Ile Glu Glu Lys Asn Ala Pro Glu Leu Gln  
 850 855 860  
 Gln Glu Ile Gln Arg Ile Leu Asn Asp Glu Val Tyr Pro Leu Arg Val  
 865 870 875 880  
 Pro Leu Glu Thr Ser Ala Phe Ile Ala Lys Arg Trp Asn Glu Leu Lys  
 885 890 895  
 Gly

## (2) INFORMATION FOR SEQ ID NO:1297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION 1...668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

```

Met Lys Lys Pro Phe Tyr Ser Leu Ser Leu Ala Ser Ser Leu Leu Asn
1          5          10          15
Ala Glu Asp Asn Gly Phe Phe Ile Ser Ala Gly Tyr Gln Ile Gly Glu
20          25          30
Ala Ala Gln Met Val Lys Asn Thr Gly Glu Leu Lys Lys Leu Ser Asp
35          40          45
Thr Tyr Glu Asn Leu Ser Asn Leu Leu Thr Asn Phe Asn Asn Leu Asn
50          55          60
Gln Ala Val Thr Asn Ala Ser Ser Pro Ser Glu Ile Asn Ala Ala Ile
65          70          75          80
Asp Asn Leu Lys Ala Asn Thr Gln Gly Leu Ile Gly Glu Lys Thr Asn
85          90          95
Ser Pro Ala Tyr Gln Ala Val Tyr Leu Ala Leu Asn Ala Ala Val Gly
100          105          110
Leu Trp Asn Val Ile Ala Tyr Asn Val Gln Cys Gly Pro Gly Asn Ser
115          120          125
Gly Gln Gln Ser Val Thr Phe Glu Gly Gln Pro Gly His Asn Ser Ser
130          135          140
Ser Ile Asn Cys Asn Leu Thr Gly Tyr Asn Asn Gly Val Ser Gly Pro
145          150          155          160
Leu Ser Ile Glu Asn Phe Lys Lys Leu Asn Gln Ala Tyr Gln Thr Ile
165          170          175
Gln Gln Ala Leu Lys Gln Asp Ser Gly Phe Pro Val Leu Asp Ser Ala
180          185          190
Gly Lys Gln Val Thr Ile Thr Ile Thr Thr Gln Thr Asn Gly Ala Asn
195          200          205
Lys Ser Glu Thr Thr Thr Thr Thr Thr Thr Thr Asn Asp Ala Gln Thr
210          215          220
Leu Leu Gln Glu Ala Ser Lys Met Ile Ser Val Leu Thr Thr Asn Cys
225          230          235          240
Pro Trp Val Asn His Asn Gln Gly Gln Asn Gly Gly Ala Pro Trp Gly
245          250          255
Leu Asp Thr Ala Gly Asn Val Cys Gln Val Phe Ala Thr Glu Phe Ser
260          265          270
Ala Val Thr Ser Met Ile Lys Asn Ala Gln Glu Ile Val Thr Gln Ala
275          280          285
Gln Ser Leu Asn Gln Gln Asn Asn Gln Asn Ala Pro Gln Asp Phe Asn
290          295          300
Pro Tyr Thr Ser Ala Asp Arg Ala Phe Ala Gln Asn Met Leu Asn His
305          310          315          320
Ala Gln Ala Gln Ala Lys Ile Leu Glu Leu Ala Asp Gln Met Lys Lys
325          330          335
Asp Leu Asn Thr Ile Pro Ser Gln Phe Ile Thr Asn Tyr Leu Ala Ala
340          345          350
Cys His Asn Gly Gly Gly Thr Leu Pro Asp Ala Gly Val Thr Asn Asn

```

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355	360	365
Thr Trp Gly Ala Gly Cys	Ala Tyr Val Glu Glu Thr	Ile Thr Ala Leu
370	375	380
Asn Asn Ser Leu Ala His	Phe Gly Thr Gln Ala Glu	Gln Ile Lys Gln
385	390	395
Ser Glu Leu Leu Ala Arg	Thr Ile Leu Asp Phe Arg	Gly Ser Leu Ser
405	410	415
Asn Leu Asn Asn Thr Tyr	Asn Ser Ile Thr Thr Thr	Ala Ser Asn Thr
420	425	430
Pro Asn Ser Pro Phe Leu	Lys Asn Leu Ile Ser Gln	Ser Thr Asn Pro
435	440	445
Asn Asn Pro Gly Gly Leu	Gln Ala Val Tyr Gln Val	Asn Gln Ser Ala
450	455	460
Tyr Ser Gln Leu Leu Ser	Ala Thr Gln Glu Leu Gly	His Asn Pro Phe
465	470	475
Arg Arg Val Gly Leu Ile	Ser Ser Gln Thr Asn Asn	Gly Ala Met Asn
485	490	495
Gly Ile Gly Val Gln Val	Gly Tyr Lys Gln Phe Phe	Gly Glu Lys Arg
500	505	510
Arg Trp Gly Leu Arg Tyr	Tyr Gly Phe Phe Asp Tyr	Asn His Ala Tyr
515	520	525
Ile Lys Ser Ser Phe Phe	Asn Ser Ala Ser Asp Val	Phe Thr Tyr Gly
530	535	540
Val Gly Thr Asp Val Leu	Tyr Asn Phe Ile Asn Asp	Lys Thr Thr Lys
545	550	555
Asn Ser Lys Ile Ser Phe	Gly Val Phe Gly Gly Ile	Ala Leu Ala Gly
565	570	575
Thr Ser Trp Leu Asn Ser	Gln Tyr Val Asn Leu Ala	Thr Phe Asn Asn
580	585	590
Phe Tyr Ser Ala Lys Met	Asn Val Ala Asn Phe Gln	Phe Leu Phe Asn
595	600	605
Leu Gly Leu Arg Met Asn	Leu Ala Lys Asn Lys Lys	Lys Ala Ser Asp
610	615	620
His Ala Ala Gln His Gly	Val Glu Leu Gly Val Lys	Ile Pro Thr Ile
625	630	635
Asn Thr Asn Tyr Tyr Ser	Leu Leu Gly Thr Gln Leu	Gln Tyr Arg Arg
645	650	655
Leu Tyr Ser Val Tyr Leu	Asn Tyr Val Phe Ala Tyr	
660	665	

## (2) INFORMATION FOR SEQ ID NO:1298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION 1...637

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

```

Met Lys Arg Gln Phe Tyr Ser Leu Ser Leu Ser Leu Ala Ser Ser Leu
1      5      10      15
Leu His Ala Glu Asp Asn Gly Phe Phe Val Ser Ala Gly Tyr Gln Ile
      20      25      30
Gly Glu Ala Val Gln Met Val Lys Asn Thr Gly Glu Leu Lys Asn Leu
      35      40      45
Asn Asp Lys Tyr Glu Gln Leu Ser Gln Ser Leu Ala Gln Leu Ala Ser
      50      55      60
Leu Lys Lys Ser Ile Gln Thr Ala Asn Asn Ile Gln Ala Val Asn Asn
65      70      75      80
Ala Leu Ser Asp Leu Lys Ser Phe Ala Ser Asn Asn His Thr Asn Lys
      85      90      95
Glu Thr Ser Pro Ile Tyr Asn Thr Ala Gln Ala Val Ile Thr Ser Val
      100      105      110
Leu Ala Phe Trp Ser Leu Tyr Ala Gly Asn Ala Leu Ser Phe His Val
      115      120      125
Thr Gly Leu Asn Asp Gly Ser Asn Ser Pro Leu Gly Arg Ile His Arg
      130      135      140
Asp Gly Asn Cys Thr Gly Leu Gln Gln Cys Phe Met Ser Lys Glu Thr
145      150      155      160
Tyr Asp Lys Met Lys Thr Leu Ala Glu Asn Leu Gln Lys Ala Gln Gly
      165      170      175
Asn Leu Cys Ala Leu Ser Glu Cys Ser Ser Asn Gln Ser Asn Gly Gly
      180      185      190
Lys Thr Ser Met Thr Thr Ala Leu Gln Thr Ala Gln Gln Leu Met Asp
      195      200      205
Leu Ile Glu Gln Thr Lys Val Ser Met Val Trp Lys Asn Ile Val Ile
      210      215      220
Ala Gly Val Thr Asn Lys Pro Asn Gly Ala Gly Ala Ile Thr Ser Thr
225      230      235      240
Gly His Val Thr Asp Tyr Ala Val Phe Asn Asn Ile Lys Ala Met Leu
      245      250      255
Pro Ile Leu Gln Gln Ala Leu Thr Leu Ser Gln Ser Asn His Thr Leu
      260      265      270
Ser Thr Gln Leu Gln Ala Arg Ala Met Gly Ser Gln Thr Asn Arg Glu
      275      280      285
Phe Ala Lys Asp Ile Tyr Ala Leu Ala Gln Asn Gln Lys Gln Ile Leu
      290      295      300
Ser Asn Ala Ser Ser Ile Phe Asn Leu Phe Asn Ser Ile Pro Lys Asp
305      310      315      320
Gln Leu Lys Tyr Leu Glu Asn Ala Tyr Leu Lys Val Pro His Leu Gly
      325      330      335
Lys Thr Pro Thr Asn Pro Tyr Arg Gln Asn Val Asn Leu Asn Lys Glu
      340      345      350
Ile Asn Ala Val Gln Asp Asn Val Ala Asn Tyr Gly Asn Arg Leu Asp
      355      360      365
Ser Ala Leu Ser Val Ala Lys Asp Val Tyr Asn Leu Lys Ser Asn Gln
      370      375      380
Thr Glu Ile Val Thr Thr Tyr Asn Asp Ala Lys Asn Leu Ser Glu Glu
385      390      395      400
Ile Ser Lys Leu Pro Tyr Asn Gln Val Asn Val Thr Asn Ile Val Met
      405      410      415
Ser Pro Lys Asp Ser Thr Ala Gly Gln Tyr Gln Ile Asn Pro Glu Gln
      420      425      430

```



Gln Ser Asn Leu Asn Gln Ala Leu Ala Ala Met Ser Asn Asn Pro Phe  
           435                                  440                                  445  
 Lys Lys Val Gly Met Ile Ser Ser Gln Asn Asn Asn Gly Ala Leu Asn  
           450                                  455                                  460  
 Gly Leu Gly Val Gln Val Gly Tyr Lys Gln Phe Phe Gly Glu Ser Lys  
 465                                  470                                  475                                  480  
 Arg Trp Gly Leu Arg Tyr Tyr Gly Phe Phe Asp Tyr Asn His Gly Tyr  
                                   485                                  490                                  495  
 Ile Lys Ser Ser Phe Phe Asn Ser Ser Ser Asp Ile Trp Thr Tyr Gly  
                                   500                                  505                                  510  
 Gly Gly Ser Asp Leu Leu Val Asn Phe Ile Asn Asp Ser Ile Thr Arg  
                                   515                                  520                                  525  
 Lys Asn Asn Lys Leu Ser Val Gly Leu Phe Gly Gly Ile Gln Leu Ala  
           530                                  535                                  540  
 Gly Thr Thr Trp Leu Asn Ser Gln Tyr Met Asn Leu Thr Ala Phe Asn  
 545                                  550                                  555                                  560  
 Asn Pro Tyr Ser Ala Lys Val Asn Ala Ser Asn Phe Gln Phe Leu Phe  
                                   565                                  570                                  575  
 Asn Leu Gly Leu Arg Thr Asn Leu Ala Thr Ala Lys Lys Lys Asp Ser  
                                   580                                  585                                  590  
 Glu Arg Ser Ala Gln His Gly Val Glu Leu Gly Ile Lys Ile Pro Thr  
                                   595                                  600                                  605  
 Ile Asn Thr Asn Tyr Tyr Ser Phe Leu Gly Thr Lys Leu Glu Tyr Arg  
           610                                  615                                  620  
 Arg Leu Tyr Ser Val Tyr Leu Asn Tyr Val Phe Ala Tyr  
 625                                  630                                  635

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## CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* polypeptide selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.
2. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.
3. A cell comprising a recombinant expression vector of claim 2.
4. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 3 under conditions that permit expression of the polypeptide.
5. A probe comprising a nucleotide sequence consisting of at least 8 nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295 or the complement thereof.
6. An isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length, wherein the sequence is hybridizable to a nucleic acid having a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295 or the complement thereof.

7. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* polypeptide or a fragment thereof, said nucleic acid comprising a nucleotide sequence selected from the group consisting of  
5 SEQ ID NO: 1-SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274-SEQ ID NO: 327, SEQ ID NO: 329-SEQ ID NO: 364, SEQ ID NO: 366-SEQ ID NO: 405, SEQ ID NO: 407-SEQ ID NO: 472, SEQ ID NO: 475-SEQ ID NO: 491, SEQ ID NO: 983, SEQ ID NO: 984, SEQ ID NO: 987-SEQ ID NO: 1033, SEQ ID NO: 1036 and SEQ ID NO: 1293-SEQ ID NO: 1295.

10

8. A vaccine composition of claim 7, further comprising a pharmaceutically acceptable carrier.

9. A vaccine composition of claim 8, wherein the pharmaceutically  
15 acceptable carrier is an adjuvant.

10. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 7, such that treatment of *H. pylori* infection occurs.

20

11. A method of claim 10, wherein the treatment is a prophylactic treatment.

12. A method of claim 10, wherein the treatment is a therapeutic treatment.

25 13. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a probe of claim 5 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

30 (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

14. A recombinant or substantially pure preparation of an *H. pylori* polypeptide selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759,  
35 SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID

NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.

- 5           15.     A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a purified *H. pylori* polypeptide or a fragment thereof, wherein said *H. pylori* polypeptide is selected from the group consisting of SEQ ID NO: 492-SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765-SEQ ID NO: 818, SEQ ID NO: 820-SEQ ID NO: 846, SEQ ID NO: 848-SEQ ID NO: 896, SEQ ID NO: 898-SEQ ID NO: 963, SEQ ID NO: 966-SEQ ID NO: 982, SEQ ID NO: 1037, SEQ ID NO: 1038, SEQ ID NO: 1041-SEQ ID NO: 1087, SEQ ID NO: 1090 and SEQ ID NO: 1296-SEQ ID NO: 1298.

- 15           16.     A vaccine composition of claim 15, further comprising a pharmaceutically acceptable carrier.

17.     A vaccine composition of claim 16, wherein the pharmaceutically acceptable carrier is an adjuvant.

- 20           18.     A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 15, such that treatment of *H. pylori* infection occurs.

- 25           19.     A method of claim 18, wherein the treatment is a prophylactic treatment.

20.     A method of claim 18, wherein the treatment is a therapeutic treatment.

21.     An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID

NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, SEQ ID NO: 1012, SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, SEQ ID NO: 1025, SEQ ID NO: 477, SEQ ID NO: 414, SEQ ID NO: 253, SEQ ID NO: 293, SEQ ID NO: 334, SEQ ID NO: 343, SEQ ID NO: 418, SEQ ID NO: 424, and SEQ ID NO: 443.

22. The purified nucleic acid of claim 21, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, SEQ ID NO: 1032, SEQ ID NO: 259, SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, SEQ ID NO: 1295, SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID

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NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, SEQ ID NO: 1031, SEQ ID NO: 254, SEQ ID NO: 352, SEQ ID NO: 415, SEQ ID NO: 1019, SEQ ID NO: 381, SEQ ID NO: 389, SEQ ID NO: 1010, and SEQ ID NO: 1012.

5           23.     he purified nucleic acid of claim 22, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 255, SEQ ID NO: 263, SEQ ID NO: 266, SEQ ID NO: 277, SEQ ID NO: 280, SEQ ID NO: 285, SEQ ID NO: 292, SEQ ID  
10 NO: 294, SEQ ID NO: 299, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 321, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 353, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 375, SEQ ID NO: 384, SEQ ID NO: 391, SEQ ID NO: 392, SEQ ID NO: 397, SEQ ID NO: 398, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 409, SEQ ID NO: 410, SEQ ID NO: 412, SEQ  
15 ID NO: 427, SEQ ID NO: 433, SEQ ID NO: 434, SEQ ID NO: 441, SEQ ID NO: 444, SEQ ID NO: 445, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 453, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 983, SEQ ID NO: 989, SEQ ID NO: 1008, SEQ ID NO: 1011, SEQ ID NO: 1014, SEQ ID NO: 1015, SEQ ID NO: 1029, and SEQ ID NO: 1032.

20

24.     The purified nucleic acid of claim 22, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a C-terminal tyrosine cluster or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 286, SEQ ID NO: 326, SEQ ID NO: 374, SEQ ID  
25 NO: 399, SEQ ID NO: 422, SEQ ID NO: 454, SEQ ID NO: 465, SEQ ID NO: 998, SEQ ID NO: 1009, SEQ ID NO: 1023, SEQ ID NO: 1294, and SEQ ID NO: 1295.

25.     The purified nucleic acid of claim 22, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a  
30 terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 319, SEQ ID NO: 325, SEQ ID NO: 425, SEQ ID NO: 437, SEQ ID NO: 438, SEQ ID NO: 447, SEQ ID NO: 448, SEQ ID NO: 467, SEQ ID NO: 996, SEQ ID NO: 1027, and SEQ ID NO: 1031.

35

26. The purified nucleic acid of claim 21, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 354, SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, SEQ ID NO: 1022, SEQ ID NO: 463, SEQ ID NO: 281, SEQ ID NO: 988, SEQ ID NO: 411, SEQ ID NO: 407, SEQ ID NO: 1017, SEQ ID NO: 290, SEQ ID NO: 417, SEQ ID NO: 430, SEQ ID NO: 992, and SEQ ID NO: 1025.

27. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 354.

28. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 372, SEQ ID NO: 400, SEQ ID NO: 421, and SEQ ID NO: 1022.

29. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 463.

30. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 281 and SEQ ID NO: 988.

31. The purified nucleic acid of claim 26, wherein said *H. pylori* inner membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 407 and SEQ ID NO: 1017.

32. The purified nucleic acid of claim 21, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a

fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 477.

33. The purified nucleic acid of claim 21, wherein said *H. pylori* cell  
5 envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof encoded by the nucleic acid comprising a nucleotide sequence of SEQ ID NO: 414.

34. A recombinant expression vector comprising the nucleic acid of claim 21  
10 operably linked to a transcription regulatory element.

35. A cell comprising a recombinant expression vector of claim 34.

36. A method for producing an *H. pylori* polypeptide comprising culturing a  
15 cell of claim 35 under conditions that permit expression of the polypeptide.

37. An isolated nucleic acid comprising a nucleotide sequence encoding an  
*H. pylori* secreted polypeptide or a fragment thereof, said nucleic acid selected from the  
group consisting of SEQ ID NO: 355, SEQ ID NO: 1006, SEQ ID NO: 257, SEQ ID  
20 NO: 258, SEQ ID NO: 260, SEQ ID NO: 261, SEQ ID NO: 264, SEQ ID NO: 265, SEQ  
ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 275,  
SEQ ID NO: 276, SEQ ID NO: 279, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO:  
287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 295, SEQ ID  
NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 301, SEQ  
25 ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 314,  
SEQ ID NO: 315, SEQ ID NO: 323, SEQ ID NO: 338, SEQ ID NO: 342, SEQ ID NO:  
348, SEQ ID NO: 349, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 359, SEQ ID  
NO: 360, SEQ ID NO: 361, SEQ ID NO: 362, SEQ ID NO: 363, SEQ ID NO: 367, SEQ  
ID NO: 370, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 377, SEQ ID NO: 378,  
30 SEQ ID NO: 379, SEQ ID NO: 380, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO:  
394, SEQ ID NO: 395, SEQ ID NO: 396, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID  
NO: 405, SEQ ID NO: 408, SEQ ID NO: 420, SEQ ID NO: 426, SEQ ID NO: 428, SEQ  
ID NO: 429, SEQ ID NO: 432, SEQ ID NO: 439, SEQ ID NO: 442, SEQ ID NO: 451,  
SEQ ID NO: 471, SEQ ID NO: 478, SEQ ID NO: 488, SEQ ID NO: 987, SEQ ID NO:  
35 990, SEQ ID NO: 991, SEQ ID NO: 993, SEQ ID NO: 1001, SEQ ID NO: 1002, SEQ



ID NO: 1007, SEQ ID NO: 1013, SEQ ID NO: 1016, SEQ ID NO: 1018, SEQ ID NO: 1021, and SEQ ID NO: 1026.

38. The purified nucleic acid of claim 37, wherein said *H. pylori* secreted  
5 polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 355 and SEQ ID NO: 1006.

39. A recombinant expression vector comprising the nucleic acid of claim 38  
10 operably linked to a transcription regulatory element.

40. A cell comprising a recombinant expression vector of claim 39.

41. A method for producing an *H. pylori* polypeptide comprising culturing a  
15 cell of claim 40 under conditions that permit expression of the polypeptide.

42. An isolated nucleic acid comprising a nucleotide sequence encoding an  
*H. pylori* cytoplasmic polypeptide or a fragment thereof, said nucleic acid selected from  
the group consisting of SEQ ID NO: 470, SEQ ID NO: 1033, SEQ ID NO: 357, SEQ ID  
20 NO: 457, SEQ ID NO: 461, SEQ ID NO: 1030, SEQ ID NO: 345, SEQ ID NO: 383,  
SEQ ID NO: 387, SEQ ID NO: 455, SEQ ID NO: 1003, SEQ ID NO: 351, SEQ ID NO:  
416, SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID  
NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004,  
SEQ ID NO: 1020, SEQ ID NO: 1293, SEQ ID NO: 318, SEQ ID NO: 322, SEQ ID  
25 NO: 324, SEQ ID NO: 330, SEQ ID NO: 347, SEQ ID NO: 440, SEQ ID NO: 446, SEQ  
ID NO: 464, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 995, SEQ ID NO: 997,  
SEQ ID NO: 1005, SEQ ID NO: 1028.

43. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic  
30 polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 470 and SEQ ID NO: 1033.

44. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic  
35 polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid

metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 357 and SEQ ID NO: 457.

45. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 461 and SEQ ID NO: 1030.

46. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 345, SEQ ID NO: 383, SEQ ID NO: 387, SEQ ID NO: 455, and SEQ ID NO: 1003.

47. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid metabolism or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 351 and SEQ ID NO: 416.

48. The purified nucleic acid of claim 42, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 278, SEQ ID NO: 335, SEQ ID NO: 346, SEQ ID NO: 350, SEQ ID NO: 419, SEQ ID NO: 460, SEQ ID NO: 472, SEQ ID NO: 1000, SEQ ID NO: 1004, SEQ ID NO: 1020, and SEQ ID NO: 1293.

49. A recombinant expression vector comprising the nucleic acid of claim 42 operably linked to a transcription regulatory element.

50. A cell comprising a recombinant expression vector of claim 49.

51. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 50 under conditions that permit expression of the polypeptide.

52. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cellular polypeptide or a fragment thereof, said nucleic acid selected from the

group consisting of SEQ ID NO: 256, SEQ ID NO: 267, SEQ ID NO: 282, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 344,  
5 SEQ ID NO: 369, SEQ ID NO: 376, SEQ ID NO: 382, SEQ ID NO: 386, SEQ ID NO: 423, SEQ ID NO: 431, SEQ ID NO: 435, SEQ ID NO: 436, SEQ ID NO: 458, SEQ ID NO: 462, SEQ ID NO: 475, SEQ ID NO: 476, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 984, SEQ ID NO: 994, SEQ ID NO: 1024, and SEQ ID NO: 1036.

53. A recombinant expression vector comprising the nucleic acid of claim 52 operably linked to a transcription regulatory element.

15 54. A cell comprising a recombinant expression vector of claim 53.

55. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 54 under conditions that permit expression of the polypeptide.

20 56. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 21.

57. A vaccine composition of claim 56, further comprising a pharmaceutically acceptable carrier.

25

58. A vaccine composition of claim 57, wherein the pharmaceutically acceptable carrier is an adjuvant.

59. A method of treating a subject for *H. pylori* infection comprising  
30 administering to a subject a vaccine composition of claim 56, such that treatment of *H. pylori* infection occurs.

60. A method of claim 59, wherein the treatment is a prophylactic treatment.

35 61. A method of claim 59, wherein the treatment is a therapeutic treatment.

62. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 37.

5 63. A vaccine composition of claim 62, further comprising a pharmaceutically acceptable carrier.

64. A vaccine composition of claim 63, wherein the pharmaceutically acceptable carrier is an adjuvant.

10 65. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 62, such that treatment of *H. pylori* infection occurs.

15 66. A method of claim 65, wherein the treatment is a prophylactic treatment.

67. A method of claim 65, wherein the treatment is a therapeutic treatment.

20 68. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 42.

69. A vaccine composition of claim 68, further comprising a pharmaceutically acceptable carrier.

25 70. A vaccine composition of claim 69, wherein the pharmaceutically acceptable carrier is an adjuvant.

30 71. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 68, such that treatment of *H. pylori* infection occurs.

72. A method of claim 71, wherein the treatment is a prophylactic treatment.

73. A method of claim 71, wherein the treatment is a therapeutic treatment.

35 74. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 52.

75. A vaccine composition of claim 74, further comprising a pharmaceutically acceptable carrier.

5 76. A vaccine composition of claim 75, wherein the pharmaceutically acceptable carrier is an adjuvant.

77. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 74, such that treatment of *H.*  
10 *pylori* infection occurs.

78. A method of claim 77, wherein the treatment is a prophylactic treatment.

79. A method of claim 77, wherein the treatment is a therapeutic treatment.  
15

80. A purified *H. pylori* cell envelope polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID  
20 NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ  
25 ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID  
30 NO: 913, SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ  
35 ID NO: 872, SEQ ID NO: 880, SEQ ID NO: 1064, SEQ ID NO: 1066, SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID

NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898,  
SEQ ID NO: 1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO:  
1046, SEQ ID NO: 1079, SEQ ID NO: 968, SEQ ID NO: 905, SEQ ID NO: 744, SEQ  
ID NO: 784, SEQ ID NO: 825, SEQ ID NO: 834, SEQ ID NO: 909, SEQ ID NO: 915,  
5 and SEQ ID NO: 934.

81. The purified polypeptide of claim 80, wherein said *H. pylori* cell  
envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide  
or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID  
10 NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ  
ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803,  
SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO:  
882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID  
NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ  
15 ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901,  
SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO:  
932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID  
NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ  
ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO:  
20 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, SEQ ID NO: 1086, SEQ ID NO: 750, SEQ  
ID NO: 777, SEQ ID NO: 817, SEQ ID NO: 865, SEQ ID NO: 890, SEQ ID NO: 913,  
SEQ ID NO: 945, SEQ ID NO: 956, SEQ ID NO: 1052, SEQ ID NO: 1063, SEQ ID  
NO: 1077, SEQ ID NO: 1297, SEQ ID NO: 1298, SEQ ID NO: 810, SEQ ID NO: 816,  
SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO:  
25 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, SEQ ID NO: 1085, SEQ  
ID NO: 745, SEQ ID NO: 843, SEQ ID NO: 906, SEQ ID NO: 1073, SEQ ID NO: 872,  
SEQ ID NO: 880, SEQ ID NO: 1064, and SEQ ID NO: 1066.

82. The purified polypeptide of claim 81, wherein said *H. pylori* outer  
30 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a  
terminal phenylalanine residue or a fragment thereof selected from the group consisting  
of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID  
NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ  
ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818,  
35 SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO:  
857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID

NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

83. The purified polypeptide of claim 81, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 746, SEQ ID NO: 754, SEQ ID NO: 757, SEQ ID NO: 768, SEQ ID NO: 771, SEQ ID NO: 776, SEQ ID NO: 783, SEQ ID NO: 785, SEQ ID NO: 790, SEQ ID NO: 802, SEQ ID NO: 803, SEQ ID NO: 804, SEQ ID NO: 812, SEQ ID NO: 818, SEQ ID NO: 820, SEQ ID NO: 882, SEQ ID NO: 844, SEQ ID NO: 855, SEQ ID NO: 857, SEQ ID NO: 859, SEQ ID NO: 866, SEQ ID NO: 875, SEQ ID NO: 882, SEQ ID NO: 883, SEQ ID NO: 888, SEQ ID NO: 889, SEQ ID NO: 893, SEQ ID NO: 895, SEQ ID NO: 900, SEQ ID NO: 901, SEQ ID NO: 903, SEQ ID NO: 918, SEQ ID NO: 924, SEQ ID NO: 925, SEQ ID NO: 932, SEQ ID NO: 935, SEQ ID NO: 936, SEQ ID NO: 940, SEQ ID NO: 941, SEQ ID NO: 943, SEQ ID NO: 944, SEQ ID NO: 957, SEQ ID NO: 959, SEQ ID NO: 960, SEQ ID NO: 1037, SEQ ID NO: 1043, SEQ ID NO: 1062, SEQ ID NO: 1065, SEQ ID NO: 1068, SEQ ID NO: 1069, SEQ ID NO: 1083, and SEQ ID NO: 1086.

84. The purified polypeptide of claim 81, wherein said *H. pylori* outer membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide having a terminal phenylalanine residue and a C-terminal tyrosine cluster or a fragment thereof selected from the group consisting of SEQ ID NO: 810, SEQ ID NO: 816, SEQ ID NO: 916, SEQ ID NO: 928, SEQ ID NO: 929, SEQ ID NO: 938, SEQ ID NO: 939, SEQ ID NO: 958, SEQ ID NO: 1050, SEQ ID NO: 1081, and SEQ ID NO: 1085.

85. The purified polypeptide of claim 80, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 845, SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, SEQ ID NO: 1076, SEQ ID NO: 954, SEQ ID NO: 772, SEQ ID NO: 1042, SEQ ID NO: 902, SEQ ID NO: 898, SEQ ID NO:

1071, SEQ ID NO: 781, SEQ ID NO: 908, SEQ ID NO: 921, SEQ ID NO: 1046, SEQ ID NO: 1079.

86. The purified polypeptide of claim 85, wherein said *H. pylori* inner  
5 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in outer membrane and cell wall synthesis or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 845.

87. The purified polypeptide of claim 85, wherein said *H. pylori* inner  
10 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 863, SEQ ID NO: 891, SEQ ID NO: 912, and SEQ ID NO: 1076.

88. The purified polypeptide of claim 85, wherein said *H. pylori* inner  
15 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 954.

89. The purified polypeptide of claim 85, wherein said *H. pylori* inner  
20 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and adhesion or a fragment thereof selected from the group consisting of SEQ ID NO: 772 and SEQ ID NO: 1042.

90. The purified polypeptide of claim 85, wherein said *H. pylori* inner  
25 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in transport or a fragment thereof selected from the group consisting of SEQ ID NO: 898 and SEQ ID NO: 1071.

91. The purified polypeptide of claim 80, wherein said *H. pylori* cell  
30 envelope polypeptide or a fragment thereof is an *H. pylori* flagellar polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 968.

92. The purified polypeptide of claim 80, wherein said *H. pylori* cell  
35 envelope polypeptide or a fragment thereof is an *H. pylori* transport polypeptide or a fragment thereof comprising an amino acid sequence of SEQ ID NO: 905.



93. A purified *H. pylori* cellular polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 747, SEQ ID NO: 758, SEQ ID NO: 773, SEQ ID NO: 797, SEQ ID NO: 798, SEQ ID NO: 799, SEQ ID NO: 800, SEQ ID NO: 801, SEQ ID NO: 807, SEQ ID NO: 808, SEQ ID NO: 823, SEQ ID NO: 824, SEQ ID NO: 827, SEQ ID NO: 828, SEQ ID NO: 830, SEQ ID NO: 831, SEQ ID NO: 832, SEQ ID NO: 835, SEQ ID NO: 860, SEQ ID NO: 867, SEQ ID NO: 873, SEQ ID NO: 877, SEQ ID NO: 914, SEQ ID NO: 922, SEQ ID NO: 926, SEQ ID NO: 927, SEQ ID NO: 949, SEQ ID NO: 953, SEQ ID NO: 966, SEQ ID NO: 967, SEQ ID NO: 970, SEQ ID NO: 971, SEQ ID NO: 972, SEQ ID NO: 973, SEQ ID NO: 974, SEQ ID NO: 975, SEQ ID NO: 976, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 980, SEQ ID NO: 1038, SEQ ID NO: 1048, SEQ ID NO: 1078, and SEQ ID NO: 1090.

94. A purified *H. pylori* secreted polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 846, SEQ ID NO: 1060, SEQ ID NO: 748, SEQ ID NO: 749, SEQ ID NO: 751, SEQ ID NO: 752, SEQ ID NO: 755, SEQ ID NO: 756, SEQ ID NO: 759, SEQ ID NO: 761, SEQ ID NO: 763, SEQ ID NO: 765, SEQ ID NO: 766, SEQ ID NO: 767, SEQ ID NO: 770, SEQ ID NO: 774, SEQ ID NO: 775, SEQ ID NO: 778, SEQ ID NO: 779, SEQ ID NO: 780, SEQ ID NO: 782, SEQ ID NO: 786, SEQ ID NO: 787, SEQ ID NO: 788, SEQ ID NO: 789, SEQ ID NO: 791, SEQ ID NO: 792, SEQ ID NO: 793, SEQ ID NO: 794, SEQ ID NO: 795, SEQ ID NO: 796, SEQ ID NO: 805, SEQ ID NO: 806, SEQ ID NO: 814, SEQ ID NO: 829, SEQ ID NO: 833, SEQ ID NO: 839, SEQ ID NO: 840, SEQ ID NO: 849, SEQ ID NO: 850, SEQ ID NO: 851, SEQ ID NO: 852, SEQ ID NO: 853, SEQ ID NO: 854, SEQ ID NO: 858, SEQ ID NO: 861, SEQ ID NO: 862, SEQ ID NO: 864, SEQ ID NO: 868, SEQ ID NO: 869, SEQ ID NO: 870, SEQ ID NO: 871, SEQ ID NO: 879, SEQ ID NO: 881, SEQ ID NO: 885, SEQ ID NO: 886, SEQ ID NO: 887, SEQ ID NO: 892, SEQ ID NO: 894, SEQ ID NO: 896, SEQ ID NO: 899, SEQ ID NO: 911, SEQ ID NO: 917, SEQ ID NO: 919, SEQ ID NO: 920, SEQ ID NO: 923, SEQ ID NO: 930, SEQ ID NO: 933, SEQ ID NO: 942, SEQ ID NO: 962, SEQ ID NO: 969, SEQ ID NO: 979, SEQ ID NO: 1041, SEQ ID NO: 1044, SEQ ID NO: 1045, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1056, SEQ ID NO: 1061, SEQ ID NO: 1067, SEQ ID NO: 1070, SEQ ID NO: 1072, SEQ ID NO: 1075, and SEQ ID NO: 1080.

95. The purified polypeptide of claim 94, wherein said *H. pylori* secreted polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in secretion and

adhesion or a fragment thereof selected from the group consisting of SEQ ID NO: 846 and SEQ ID NO: 1060.

96. A purified *H. pylori* cytoplasmic polypeptide or a fragment thereof,  
5 wherein said polypeptide is selected from the group consisting of SEQ ID NO: 961, SEQ ID NO: 1087, SEQ ID NO: 848, SEQ ID NO: 948, SEQ ID NO: 952, SEQ ID NO: 1084, SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, SEQ ID NO: 1057, SEQ ID NO: 842, SEQ ID NO: 907, SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO:  
10 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, SEQ ID NO: 1296, SEQ ID NO: 809, SEQ ID NO: 813, SEQ ID NO: 815, SEQ ID NO: 821, SEQ ID NO: 838, SEQ ID NO: 931, SEQ ID NO: 937, SEQ ID NO: 955, SEQ ID NO: 981, SEQ ID NO: 982, SEQ ID NO: 1049, SEQ ID NO: 1051, SEQ ID NO: 1059, and SEQ ID NO: 1082.
- 15 97. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in energy conversion or a fragment thereof selected from the group consisting of SEQ ID NO: 961 and SEQ ID NO: 1087.
- 20 98. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in amino acid metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 848 and SEQ ID NO: 948.
- 25 99. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in nucleotide metabolism and transport or a fragment thereof selected from the group consisting of SEQ ID NO: 952 and SEQ ID NO: 1084.
- 30 100. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in cofactor metabolism or a fragment thereof selected from the group consisting of SEQ ID NO: 836, SEQ ID NO: 874, SEQ ID NO: 878, SEQ ID NO: 946, and SEQ ID NO: 1057.
- 35 101. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in lipid

metabolism or a fragment thereof selected from the group consisting of SEQ ID NO: 842 and SEQ ID NO: 907.

102. The purified polypeptide of claim 96, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide involved in genome replication, transcription, recombination and repair or a fragment thereof selected from the group consisting of SEQ ID NO: 769, SEQ ID NO: 826, SEQ ID NO: 837, SEQ ID NO: 841, SEQ ID NO: 910, SEQ ID NO: 951, SEQ ID NO: 963, SEQ ID NO: 1054, SEQ ID NO: 1058, SEQ ID NO: 1074, and SEQ ID NO: 1296.

10

103. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 80.

104. A vaccine composition of claim 103, further comprising a pharmaceutically acceptable carrier.

15

105. A vaccine composition of claim 104, wherein the pharmaceutically acceptable carrier is an adjuvant.

106. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 103, such that treatment of *H. pylori* infection occurs.

20

107. A method of claim 106, wherein the treatment is a prophylactic treatment.

25

108. A method of claim 106, wherein the treatment is a therapeutic treatment.

109. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 93.

30

110. A vaccine composition of claim 109, further comprising a pharmaceutically acceptable carrier.

111. A vaccine composition of claim 110, wherein the pharmaceutically acceptable carrier is an adjuvant.

35

112. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 109, such that treatment of *H. pylori* infection occurs.

5

113. A method of claim 112, wherein the treatment is a prophylactic treatment.

114. A method of claim 112, wherein the treatment is a therapeutic treatment.

10

115. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 94.

116. A vaccine composition of claim 115, further comprising a pharmaceutically acceptable carrier.

15

117. A vaccine composition of claim 116, wherein the pharmaceutically acceptable carrier is an adjuvant.

118. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 115, such that treatment of *H. pylori* infection occurs.

20

119. A method of claim 118, wherein the treatment is a prophylactic treatment.

25

120. A method of claim 118, wherein the treatment is a therapeutic treatment.

121. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 96.

30

122. A vaccine composition of claim 121, further comprising a pharmaceutically acceptable carrier.

123. A vaccine composition of claim 122, wherein the pharmaceutically acceptable carrier is an adjuvant.

35

124. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 121, such that treatment of *H. pylori* infection occurs.

5

125. A method of claim 124, wherein the treatment is a prophylactic treatment.

10

126. A method of claim 124, wherein the treatment is a therapeutic treatment.

127. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

15

(a) contacting a sample with a nucleic acid of claim 21 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

20

128. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a nucleic acid of claim 37 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

25

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

129. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising: .

30

(a) contacting a sample with a nucleic acid of claim 42 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

130. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

- (a) contacting a sample with a nucleic acid of claim 52 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

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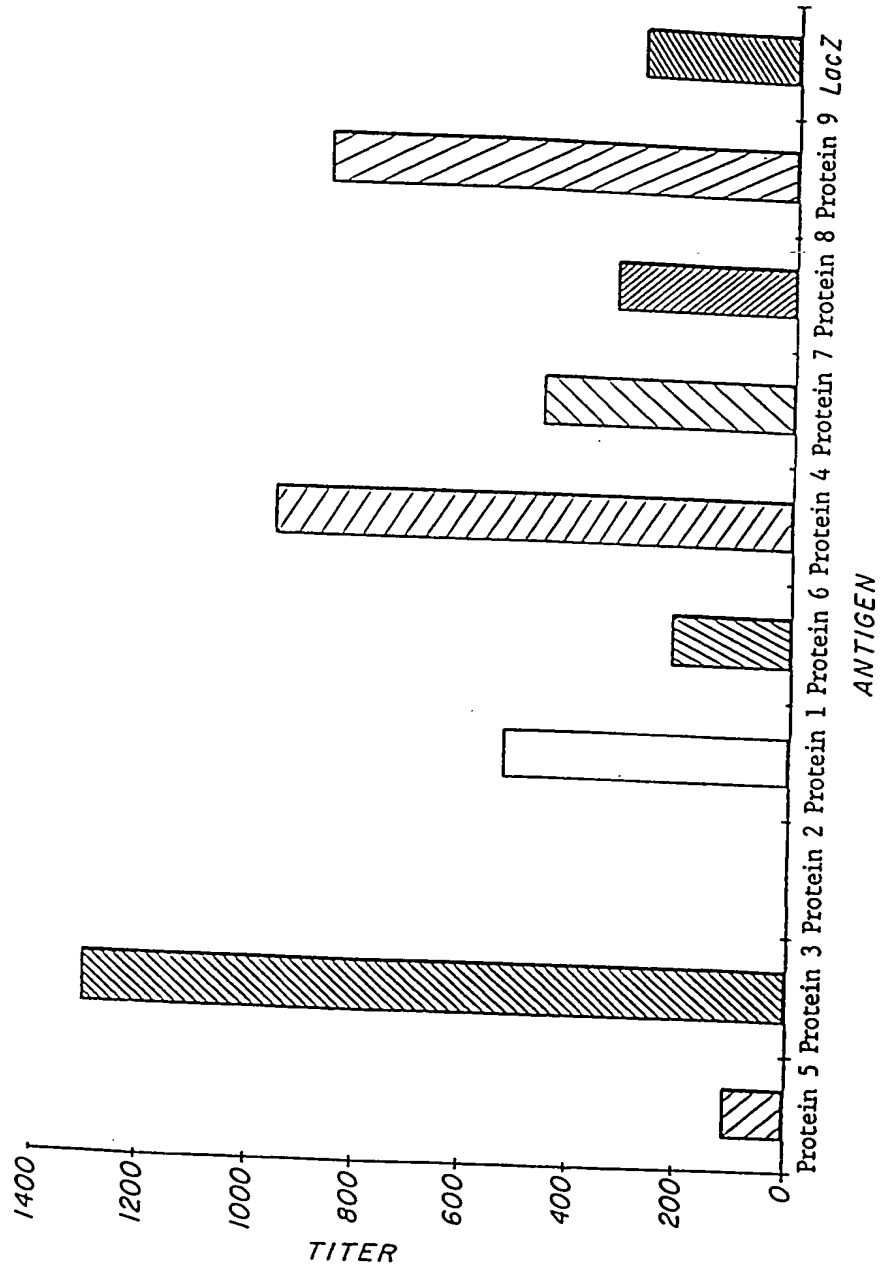


FIGURE 1

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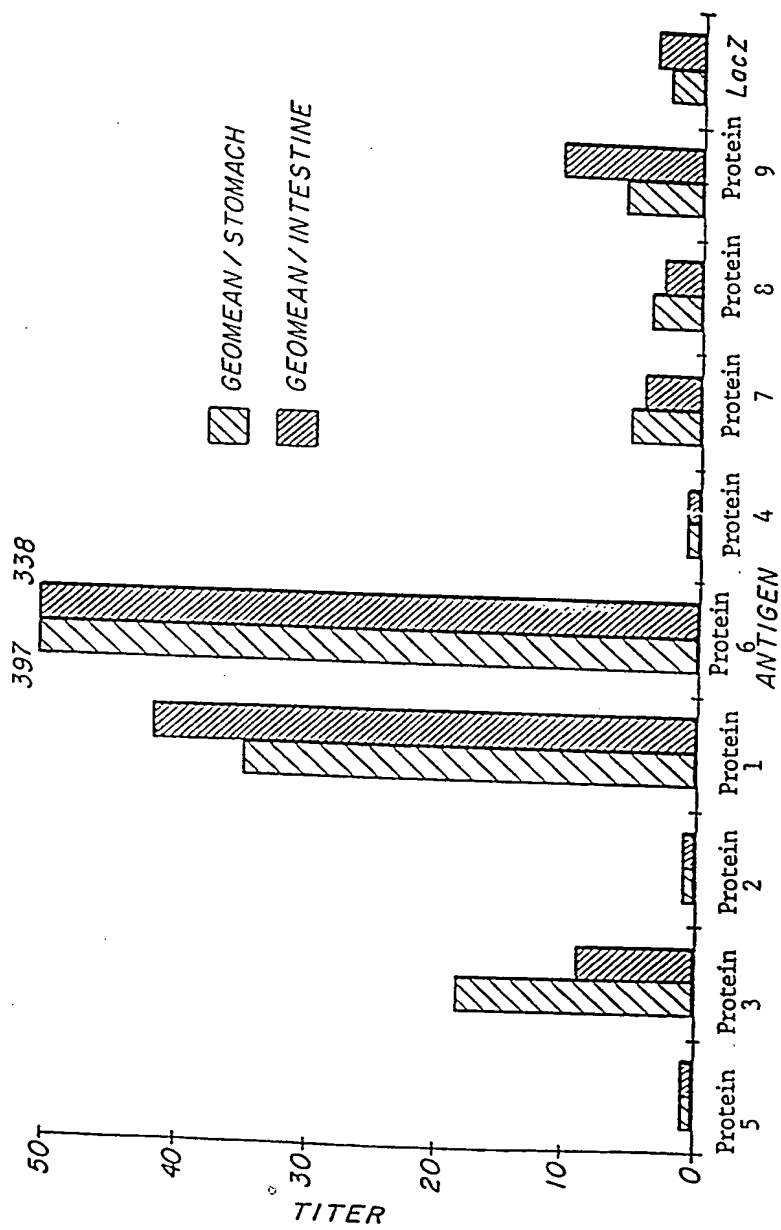


FIGURE 2



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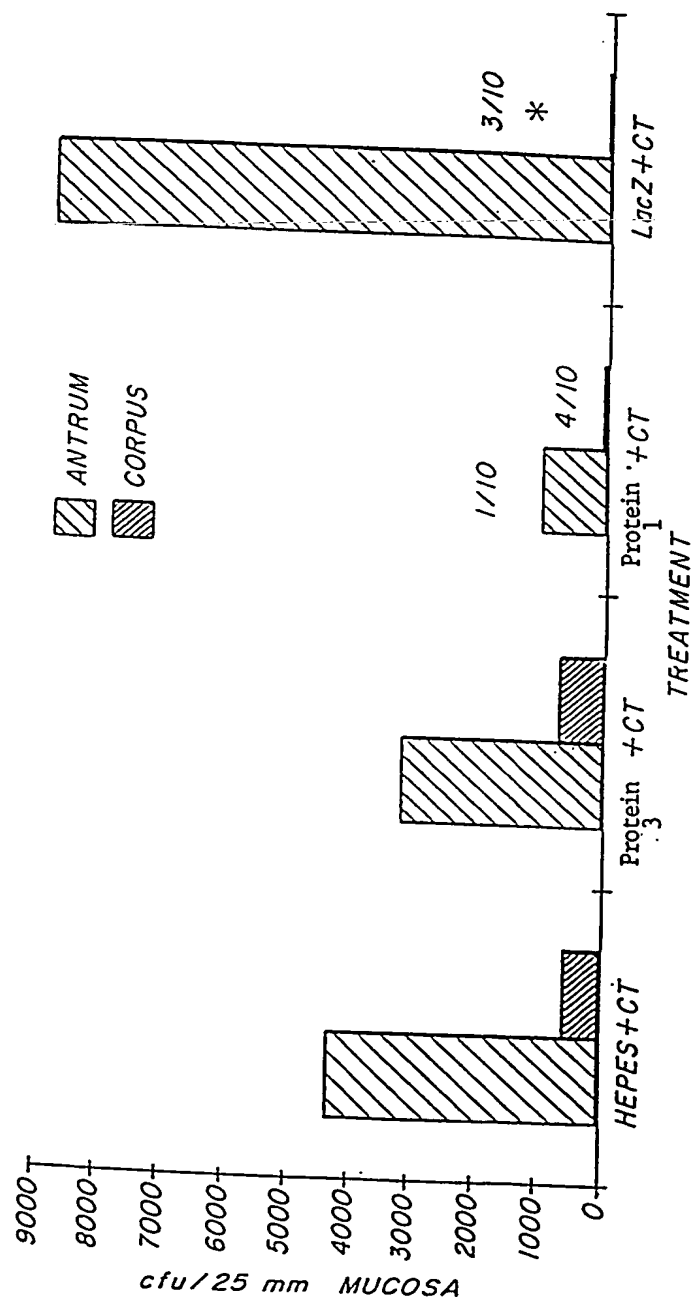


FIGURE 3

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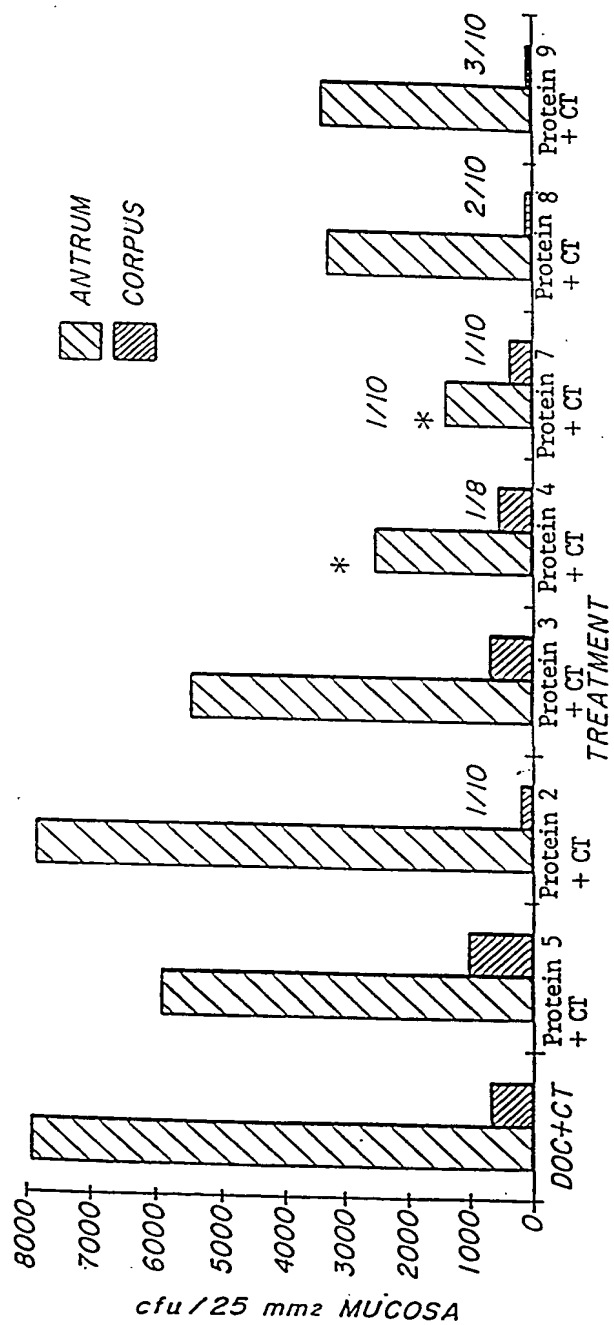
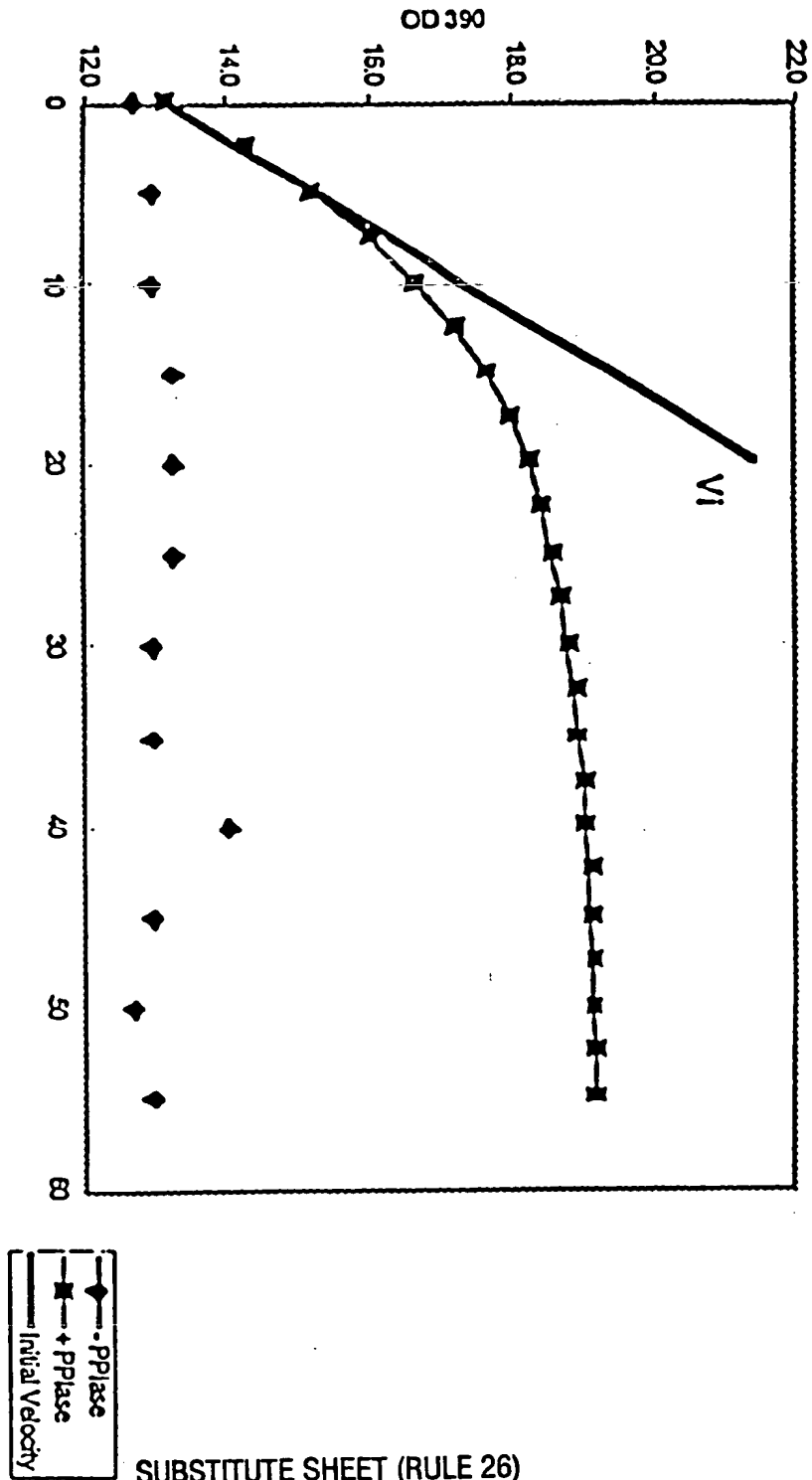


FIGURE 4

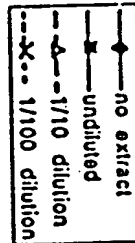
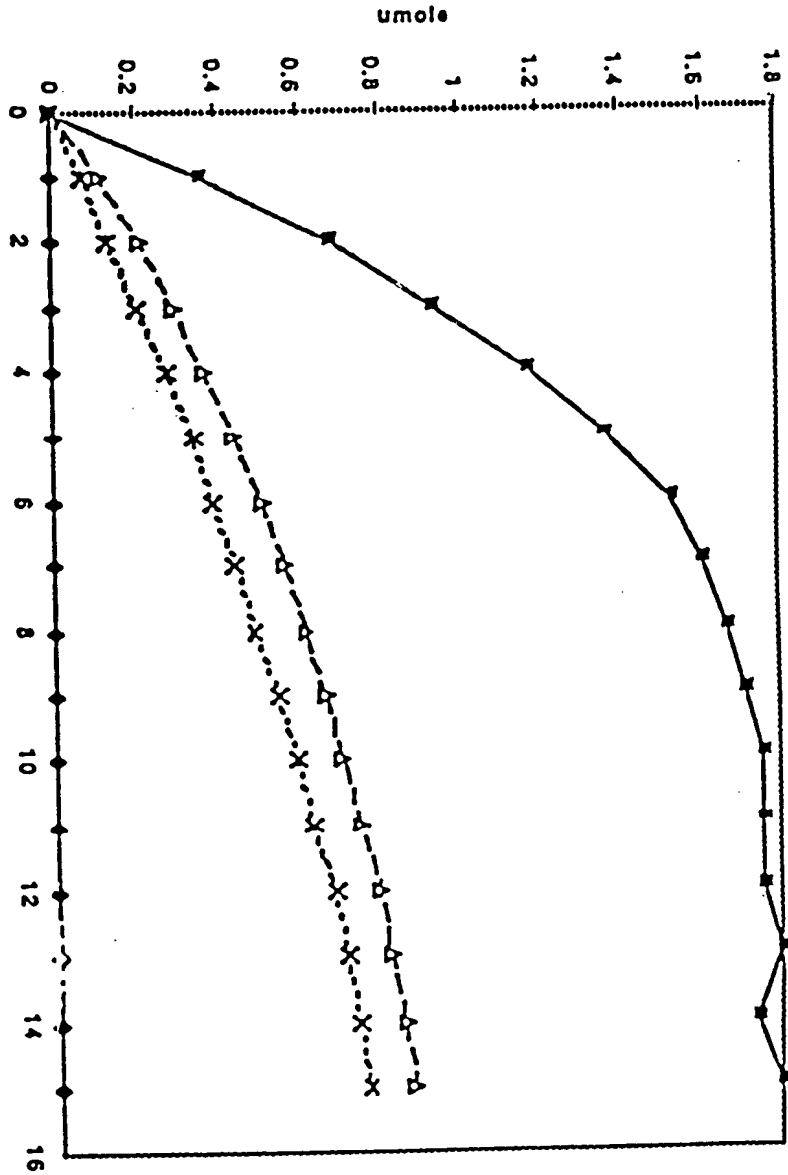
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FIGURE 5



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FIGURE 6



SUBSTITUTE SHEET (RULE 26)

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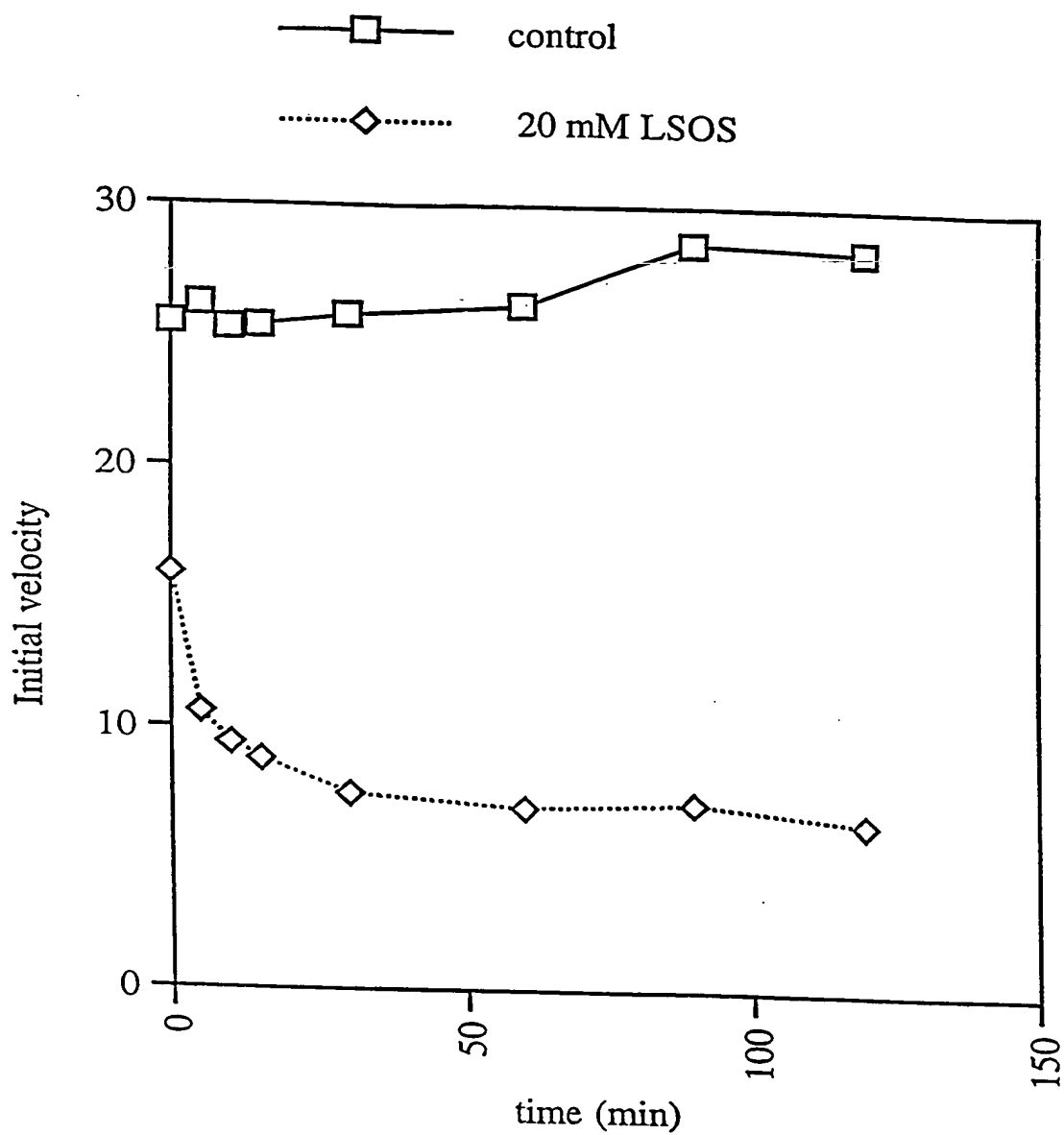


FIGURE 7

929	.RRR.....	ERTI.....	.....
938	.RGT.....	EADI.....	.....
810	.YQN.....	RSVDM.....	.....
940	.YNT.....	KALNF.....	.....
945	TRKN.....	NKLSV.....	.....
956	T.KN.....	SKISF.....	.....
433	.AQ.....	KHSSV.....	.....
777	.KE.....	GYNTA.....	.....
916	IFNR.....	ENLHL.....	.....
816	.NG.....	DAFFA.....	.....
830	ASQEVERRV	KGLSIFYKDM	TGRTLADATL KRASRHIIRK
959	.....	.....	.....RA

## FIGURE 8

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aaSeqID#:	BLOCK C	BLOCK D	BLOCK E	BLOCK F
929	.. GLFFGAQIAGQTW	STNVT NLLSQG.... RPD VKSSS	VIA.HKYFATQGSS AS.....	YMRNFSFYVGYSGVF *....
938	.. GFFAGIQLAGQTW	KTNFL DQVDGN.... HLK PKDTS	LY. HTYYQSEGV AK.....	YRRAFS FYVGYNIGF *....
810	.. GFFSGIQLAGETF	QSTLR DDPNVKL.... HGK INNTH	TIY.NTYKKSAGTT VK.....	YFRPYSVYMSYGYSF *....
940	.. GLFAGVQLGGATW	LSSLR QQIIDNW.... GNAND IHSTN	LIN.QAYLNSAGAD VS.....	YRRLYTFYINYINGF *....
945	.. GLFGIQLAGTTW	LNSQY M....NLTA F NNP...YSAK VNASN	TIN.TNYYSFLGTG LE.....	YRRLYSVYLNIVFAY *....
956	.. GVFGGIALAGTSW	LNSQY V....NLATF NNF...YSAK MNVAN	TIN.TNYYSLLGTQ LQ.....	YRRLYSVYLNIVFAY *....
433	.. GFYVGFALAGSSW	VGSGL GMVSMQDFI NNYLTDYRAK MHTSF	LAV.NSFYETHGKG LNA.....	FKRLVMFNVSYYVSF *....
777	.. GLFVGFGGLGDSF	IVQGE SYLKSQMCI NN.TAGCSAS MNTSY	LFT.NQFYKERGV D GSV.....	YKRNFSIYFNVMINL *....
916	.. GFFLGVAIGTTSW	GPTNY .....YF KDLAEYRGS FHFSN	TIR.NNYITASADN VPE.....	FHRPYAFYWRIVSF *....
816	.. GFNLGIAFAG...	...VY DRLSDALLYQ TLLQNTFGCK VNLNG	TYFNNHYYSNMNIS NNSENVLKV L RELEYGINS L LYQVD	FRNYSVFNTYTSF *....
890	SS GLVIGMELGASTW	FAS... ..NNLTPFNQV YSRTI	AFKNYSDDYGDK LD.....	YKRVSVYLNIVTYNF KNKH*
959	FG TLLILGVNFVGETW	F.... ..YETKIF KQWAKDSLNT YRPNM	FL.INDYFKTP... ..LYTLHFKR NI	SVYLTSTYDE *....
aaSeqID#:	BLOCK C	BLOCK D	BLOCK E	BLOCK F
929	.. TNFAK TNFNKH.RLD QG.....I	STNVT NLLSQG.... RPD VKSSS	VIA.HKYFATQGSS AS.....	YMRNFSFYVGYSGVF *....
938	.. TNFSK IAHQKRFRS QG.....I	KTNFL DQVDGN.... HLK PKDTS	LY. HTYYQSEGV AK.....	YRRAFS FYVGYNIGF *....
810	.. MNFGK LDGKSNRHNQ HT.....V	QSTLR DDPNVKL.... HGK INNTH	TIY.NTYKKSAGTT VK.....	YFRPYSVYMSYGYSF *....
940	.. TNFAE FKRFAKKFHN QGVISQKSV	LSSLR QQIIDNW.... GNAND IHSTN	LIN.QAYLNSAGAD VS.....	YRRLYTFYINYINGF *....
945	.. TNLAT AKKDSERSA QH....GV	LNSQY M....NLTA F NNP...YSAK VNASN	TIN.TNYYSFLGTG LE.....	YRRLYSVYLNIVFAY *....
956	.. MNLAK NKKKASDHAA QH....GV	LNSQY V....NLATF NNF...YSAK MNVAN	TIN.TNYYSLLGTQ LQ.....	YRRLYSVYLNIVFAY *....
433	.. VNVD R .....HN....GF	VGSGL GMVSMQDFI NNYLTDYRAK MHTSF	LAV.NSFYETHGKG LNA.....	FKRLVMFNVSYYVSF *....
777	.. SNFSK .....HS....GI	IVQGE SYLKSQMCI NN.TAGCSAS MNTSY	LFT.NQFYKERGV D GSV.....	YKRNFSIYFNVMINL *....
916	.. LG... ..TK HQ....GF	GPTNY .....YF KDLAEYRGS FHFSN	TIR.NNYITASADN VPE.....	FHRPYAFYWRIVSF *....
816	.. LGNEH NQ.....F	...VY DRLSDALLYQ TLLQNTFGCK VNLNG	TYFNNHYYSNMNIS NNSENVLKV L RELEYGINS L LYQVD	FRNYSVFNTYTSF *....
890	.. FSS DEYDIDRYGD ENYLGSSV	FAS... ..NNLTPFNQV YSRTI	AFKNYSDDYGDK LD.....	YKRVSVYLNIVTYNF KNKH*
959	.. YRFSR YKN.....WAI	F.... ..YETKIF KQWAKDSLNT YRPNM	FL.INDYFKTP... ..LYTLHFKR NI	SVYLTSTYDE *....

FIGURE 8 (CONTINUED)

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aaSeqID#:

810	MQQQLTYLNAGNVFFNAMNKA	LEKNGTA	TANSTSSTSGATGSDG
925	MQFQKTLLSLSLLFLSYCI	AEENGAY	ASVGFEYSISHAVEHN
929	LKNHSFKKTIALSLLASMSLCN	AEEDGAF	FVIDYQTSLARQELKN
938	LQNFVFNKKWLIYSSLLPLFFLNPLM	AEDDGFF	MGVSYQTS LAVQRVDN
956	KKPFYSLSLASSLLN	AEDNGFF	ISAGYQIGEAQMVKV
945	LH	AEDNGFF	VSAGYQIGEAQMVKV
940	MIKKAKKFIPFLIGSLL	AEDNGWY	MSVGYQIGGTQQFINN
890	MKKVLLLTLSLSLSFWLH	AERNIFY	LGLNFAEGSYIQGQGS
777	MKKIFLGMALAFSVSM	AEKSGAF	LGGGFQYSNLENQNTT

FIGURE 9



## INTERNATIONAL SEARCH REPORT

International Application No.  
PCT/US97/05223

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12Q 1/68; A01N 43/04; A61K 31/70

US CL : 435/6; 514/44

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 514/44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

genbank, dialog

search terms: specific SEQ ID No's and helicobacter pylori

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim N .
A	BUKANOV, N.O. et al. Ordered cosmid library and high-resolution physical-genetic map of <i>Helicobacter pylori</i> strain NCTC11638. Molecular Microbiology. February 1994, Vol. 11, No. 3, page 509-523, see whole article.	1, 5-7, 14-15, 21-23, 39, 40-41, 43-44, 61-63, 67-69, 77-79, 83-85
A	TAYLOR, D.E. et al. Construction of a <i>Helicobacter pylori</i> genome map and demonstration of diversity at the genome level. Journal of Bacteriology. November 1992, Vol. 174, No. 21, pages 6800-6806, especially pages 6802-6803.	1, 5-7, 14-15, 21-23, 39, 40-41, 43-44, 61-63, 67-69, 71, 77-79, 83-85

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"B" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Z" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

14 JULY 1997

Date of mailing of the international search report

05 AUG 1997

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

GINNY PORTNER

Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)\*

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05223

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Extra Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:  
1-130(in part, elected SEQ ID NOs as noted in response to 206)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☒

No protest accompanied the payment of additional search fees.

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):

This International Search Authority has found 309 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-13, 21-79 and 127-130 are directed to no fewer than 620 DNAs, vectors containing the different DNAs, organisms transformed with the DNAs, DNA encoding fragments of the polypeptides encoded by the no fewer than 620 different DNAs, vaccines and methods of producing the polypeptides encoded by the no fewer than 620 different DNAs.

Group II, claims 14-20 and 80-126 are drawn to no fewer than 620 different polypeptides encoded by a subset of the encoding DNAs mentioned in Group I.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows:

Group I contains a separate DNA species for each sequence mentioned. Therefore, there is a minimum of 620 species. Group II contains at least one polypeptide for each DNA sequence mentioned. Therefore, this is a minimum of 620 species in Group II.

For either Group that applicant elects, a total of 10 (ten) specified sequences will be searched and no more than 4 (four) specified sequences will be searched for each additional fee paid; if no additional fee is paid and no election indicated the first 10 sequences will be searched.

and it considers that the International Application does not comply with the requirements of unity of invention (Rules 13.1, 13.2 and 13.3) for the reasons indicated below:

The polypeptide encoding DNAs, vectors containing them, organisms transformed with them and methods of polypeptide production using them are materially different from and are therefore independent from the polypeptides of Group II. Additionally, none of the products or methods of Group I is needed to make the polypeptides of Group II.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: There is no relationship between or among the various nucleotide and amino acid sequences mentioned in the claims.

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